

II. REMARKS

Formal Matters

The specification is amended to refer to sequence identifiers. Support for the amendments is found in the specification and figures at, inter alia, Example 1, section A, page 15. Accordingly, no new matter is introduced by the amendments to the specification.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached is captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

Applicants respectfully entry of the above-noted amendments to the specification.

Objections to the specification

This communication is responsive to the Office Action which issued on September 13, 2001. The Office Action stated that the instant specification does not comply with the requirements of 37 C.F.R. §1.821-1.825. Applicants respectfully request the above-noted amendments to the specification.

Sequence Listing

A new Sequence Listing is provided herewith, which is in compliance with the requirements of 37 C.F.R. §1.821-1.825. No new matter is added.

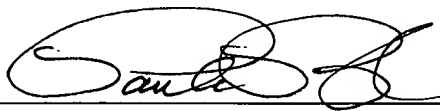
III. CONCLUSION

If the Examiner finds that a telephone conference would expedite the prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-0815, order number GRUE-003.

Respectfully submitted,
BOZICEVIC, FIELD & FRANCIS LLP

Date: Oct. 12, 2001

By: 
Paula A. Borden
Registration No. 42,344

BOZICEVIC, FIELD & FRANCIS LLP
200 Middlefield Road, Suite 200
Menlo Park, CA 94025
Telephone: (650) 327-3400
Facsimile: (650) 327-3231

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Please enter the following amendments to the specification.

Please amend page 14, line 2, as follows:

[Total sequencing of gp190^S] Figure 3C provides the native nucleotide sequence (gp190ⁿ; SEQ ID NO:1) encoding gp190; the synthetic nucleotide sequence (gp190^s; SEQ ID NO:2) encoding gp190; and the amino acid (SEQ ID NO:3) of gp190.

Please amend page 14, line 3, as follows:

N- and C-termini of gp190^{S1} and gp190^{S2} variants [variant]

Please amend page 16, line 16, as follows:

D. N- and C-termini of gp190^{S1} and gp190^{S2} variants [variant] (see Fig. 3D)

Please amend the paragraph beginning on page 16, line 22, as follows:

The N-terminal and C-terminal sequences of gp120^{S1} are provided as SEQ ID NO:4 and SEQ ID NO:5, respectively. Figure 3D depicts nucleotides 1-17 and 4863-4894 of SEQ ID NO:4 and amino acids 1-3 and 1619-1621 of SEQ ID NO:5. The N-terminal sequence of gp120^{S2}, beginning with the BamHI cleavage site, indicates the transition at amino-acid 20, from which it can be assumed that after splitting of the signal peptide it defines the N-terminus. At the C-terminus the sequence encoded ended at amino-acid 1621. The stop-codon followed the ClaI cleavage site. The nucleotide and amino acid sequences of gp120^{S2} are provided as SEQ ID NO:6 and SEQ ID NO:7, respectively. Figure 3D depicts nucleotides 1-17 and 4806-4838 of SEQ ID NO:6 and amino acids 1-3 and 1600-1602 of SEQ ID NO:7.

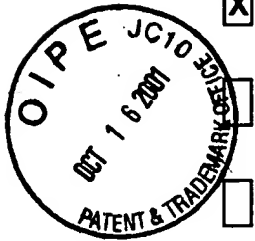
Please amend the paragraph beginning on page 17, line 3, as follows:

The gp120^{S2} sequence was inserted via the BamHI and ClaI cleavage sites into pDS56RBSII, by means of which 6 histidine as well as some amino-acids originating in the vector were fused to the N-terminus. This produces the following N-terminal sequence on the reading-frame:

MetArgGlySer(His)₆GlySer (SEQ ID NO:8). Through the promoter P_{N25lac0-1} the transcription comes under lacR/O/IPTG control.

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: All disclosed sequences are not listed as required by 37 CFR § 1.821(c), because the sequences disclosed at least on page 17, line 6, and in Fig. 3D do not appear in either the CRF or the paper copy of the "Sequence Listing". Also, "SEQ ID NO:" identifiers must be entered as required by 37 CFR § 1.821(d).

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).
- ☒ Amendments to the specification directing entry of "SEQ ID NO:" identifiers into the specification.

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

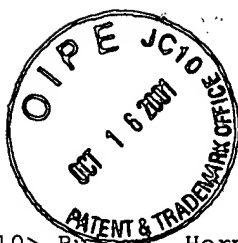
For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE



RECEIVED

OCT 22 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Bujaard, Hermann

<120> Recombinant Process for Preparing a Complete Malaria Antigen, GP190/MSP1

<130> GRUE-003

<140> 09/269,874

<141> 1999-08-02

<150> PCT/EP97/05441

<151> 1997-10-02

<150> DE 19640817.2

<151> 1996-10-02

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4920

<212> DNA

<213> Plasmodium falciparum

<400> 1

atgaagatca	tattcttttt	atgttcattt	ctttttttta	ttataaatac	acaatgtgta	60
acacatgaaa	gttatcaaga	acttgtcaaa	aaactagaag	ctttagaaga	tgacgtattg	120
acagggtata	gtttatttca	aaaggaaaaa	atggtattaa	atgaaggaa	aagtggaa	180
gctgttacaa	ctagtagacc	tggttcaaa	gggttcaggt	cttcagggtg	ttcagggtgg	240
tcagttgctt	cagggtggct	agttgcttca	gggtggctcag	ttgcttcagg	tggttcagtt	300
gcttcagggt	gttcaggtaa	ttcaagacgt	acaaatcctt	cagataattc	aagtgattca	360
gatgctaaa	cttagcgtga	tttaaaacac	agagtacgaa	attacttggt	aactatcaaa	420
gaactcaaat	ttctcaact	ctttgattta	actaatcata	tgtaacttt	gtgtgataat	480
attcatgggt	tcaaatattt	aattgatgga	tatgaagaaa	ttaatgaatt	attatataaa	540
ttaaactttt	attttgattt	attaagagca	aaattaaatg	atgtatgtgc	taatgattat	600
tgtcaaatac	ctttcaatct	taaaattcgt	gcaaataaat	tagacgtact	taaaaaactt	660
gtgttcggat	atagaaaacc	attagacaat	attaaagata	atgtaggaaa	aatggaagat	720
tacattaaaa	aaaataaaaa	aaccatagaa	aataataaat	aattaattga	agaaagtaag	780
aaaacaattg	ataaaaaata	gaatgcaact	aaagaagaag	aaaaaaaaaa	attataccaa	840
gctcaatatg	atcttttctat	ttacaataaa	caattagaag	aagcacataa	tttaataagc	900
gttttagaaa	aacgtattga	cacttttaaa	aaaaatgaaa	acattaagga	attacttgat	960
aagataaatg	aaattaaaaa	tccccaccg	gccaattctg	gaaatacacc	aaatactctc	1020
cttgataaga	acaaaaaaat	cgagggaacac	gaaaaagaaa	taaaagaaat	tgccaaaact	1080
attaaattta	atattgatag	tttattttact	gatccacttg	aattagaata	ctattttaaga	1140
gaaaaaaata	aaaatattga	tataagtgc	aagggtgaaa	caaagggaatc	aactgaaccc	1200
aatgaatatc	caaatggagt	tacttatcct	ttgtcatata	acgatattaa	caatgcttta	1260
aatgaactta	attcttttgg	tgatttaatt	aatccatttg	attatacaaa	agaaccaagt	1320
aaaaacatat	atactgataa	tgaaagaaaa	aaattcataa	atgaaattaa	ggaaaaaatt	1380
aaaatagaaa	aaaaaaaaa	tgaatctgat	aaaaaatctt	acgaagacag	atctaagtct	1440
ttaatgata	taacaaaaga	atatgaaaaa	ttacttaatg	aaatttatga	tagcaaatc	1500
aaataataa	tagatttaac	taatttcgaa	aaaatgatgg	gtaaaagata	ttcatataaa	1560
gttgagaaac	ttacacacca	taatactttt	gcacccatg	aaaattctaa	acataatctt	1620

gaaaagttaa	caaaagctct	taaatatatg	gaagattatt	ctttaaggaa	tatagtagtt	1680
gaaaaagaat	taaaatatta	taaaaattta	ataagcaaaa	tagaaaatga	gattgaaaca	1740
ttagttgaaa	atattaaaaa	agatgaagaa	cagctttttg	aaaaaaaaat	tactaaagac	1800
gaaaataaac	cagatgaaaa	aatttttagaa	gtatctgaca	ttgtaaaagt	acaagttcaa	1860
aaagttttat	taatgaacaa	aattgacgaa	ttaaaaaaga	ctcaattgat	tttaaaaaat	1920
gtagaattaa	aacataatat	acatgttccc	aattccttaca	aacaagaaaa	taagcaagaa	1980
ccttattatt	taattgtggt	gaaaaaagaa	attgataaat	taaaagtgtt	catgcctaag	2040
gtagaatcat	tgataaatga	agaaaaaaaa	aacataaaaa	cagaaggtca	atcggataat	2100
tcggaaccat	caaccgaagg	agaaataaca	ggacaagcaa	ctacaaaacc	tggacaacaa	2160
gcaggatctg	ctttagaagg	agattcagta	caagcacaa	cacaagaaca	aaaacaagca	2220
caaccaccag	taccagtacc	agtaccagaa	gcaaaagcac	aagtcccaac	accaccagca	2280
ccagtaaata	ataaaactga	aaatgtttcc	aaattagatt	atcttgaaaa	attatatgaa	2340
tttttaaata	cttcataatat	atgtcacaaa	tatatatttg	tttcacactc	aactatgaac	2400
gaaaagatat	taaaacaata	taaaattaca	aaggaggaag	aaagcaaatt	aagttcatgt	2460
gatccattag	acttattggt	taatatacaa	aataacatac	ctgtaatgta	ttctatgttt	2520
gatagcttaa	acaatagttt	atcacaaacta	tttatggaaa	tttatgaaaa	agaaatggtt	2580
tgtaatttat	ataaacttaa	ggataatgac	aaaattaaaa	atttattaga	ggaagcgaaa	2640
aaagtatcca	catctgtaaa	aactctttca	agttcatcaa	tgcaaccatt	atcattaaca	2700
cctcaggata	aacccgaagt	aagtgcacaa	agtatacat	cacattctac	aaatttgaat	2760
aatagtttaa	aattatttga	aaacatatatt	agtcttgga	aaaacaaaaa	tatatacca	2820
gaattaatag	gtcaaaaaag	tagtgaaaac	ttttatgaaa	agatattaaa	agatagtgat	2880
acattttata	atgaatcttt	tacaaatttt	gtaaaatcta	aagctgatga	tattaattca	2940
ttgaatgatg	aatcaaaaag	gaagaaatta	gaagaagata	ttaataaatt	aaaaaaaaact	3000
ttacagttat	catttgattt	atataataaa	tataaattaa	aattagaaa	attatttgat	3060
aaaaagaaaa	cagtttgtaa	atataaaatg	caaattaaaa	aacttacttt	attaaaagaa	3120
caattagaat	caaaattgaa	ttcacttaat	aacccaaagc	atgtattaca	aaacttttct	3180
gttttcttta	acaaaaaaa	agaagctgaa	atagcagaaa	ctgaaaacac	attagaaaa	3240
acaaaaatat	tattgaaaca	ttataaagga	cttgttaaat	attataatgg	tgaatcatct	3300
ccattaaaaa	ctttaagtga	agaatcaatt	caaacagaag	ataattatgc	cagtttagaa	3360
aacttttaa	tattaagtaa	attagaagga	aaattaaagg	ataattttaa	tttagaaaag	3420
aaaaaattat	catacttatc	aagtggatta	catcatttaa	ttgctgaatt	aaaagaagta	3480
ataaaaaata	aaaattatac	aggtaattct	ccaagtga	ataatacgg	tgtaacaat	3540
gcattagaat	cttacaaaa	atcttcccca	gaaggaacag	atgttgcaac	agttgtaagt	3600
gaaagtggat	ccgacacatt	agaacaaagt	caaccaaaga	aaccagcatc	aactcatgta	3660
ggagcagagt	ctaacacaat	aacaacatca	caaaatgtcg	atgatgaagt	agatgacgta	3720
atcatagtag	ctatatgttg	agaatccgaa	gaagattatg	atgatttagg	acaagtagta	3780
acaggagaag	cagtaactcc	ttccgtaatt	gataacatac	tttctaaaat	tgaaaatgaa	3840
tatgagggtt	tatatattaa	accttttagca	ggtgtttata	gaagttttaa	aaaacaatta	3900
gaaaataacg	ttatgacatt	taatgttaat	gttaaggata	ttttaaattc	acgattta	3960
aaacgtgaaa	atttcaaaa	tgtttttagaa	tcagatttaa	ttccatata	agatttaaca	4020
tcaagtaatt	atgttgtcaa	agatccatat	aaatttctta	ataaagaaaa	aagagataaa	4080
ttcttaagca	gttataatta	tattaaggat	tcaatagata	cggatataaa	ttttgcaaat	4140
gatgttcttg	gatattataa	aatattatcc	gaaaaatata	aatcagattt	agattcaatt	4200
aaaaaatata	tcaacgacaa	acaaggtgaa	aatgagaaat	accttccctt	tttaacaat	4260
attgagacct	tatataaaa	agttaatgat	aaaattgatt	tatttgta	tcatttagaa	4320
gcaaaagtcc	taaattatac	atatgagaaa	tcaaacgtag	aagttaaaat	aaaagaactt	4380
aattacttaa	aaacaattca	agacaaattg	gcagatttta	aaaaaaata	caatttcggt	4440
ggaattgctg	atttatcaac	agattataac	cataataact	tattgacaaa	gttccttagt	4500
acaggtagtg	tttttgaaaa	tcttgctaaa	accgttttat	ctaatttact	tgatggaaac	4560
ttgcaaggta	tgttaaacat	ttcacaacac	caatgcgtaa	aaaaacaatg	tccacaaaat	4620
tctggatggt	tcagacattt	agatgaaaga	gaagaatgta	aatgtttatt	aaattacaaa	4680
caagaagggtg	ataaatgtgt	tgaaaatcca	aatcctactt	gtaacgaaaa	taatggtgga	4740
tgtgatgcag	atgccaaatg	taccgaagaa	gattcaggta	gcaacggaaa	gaaaatcaca	4800
tgtgaatgta	ctaaacctga	ttcttatcca	cttttcgatg	gtattttctg	cagttcctct	4860
aacttcttag	gaatatcatt	cttattaata	ctcatgttaa	tattatacac	tttcatttaa	4920

<210> 2
 <211> 4940
 <212> DNA
 <213> Plasmodium falciparum

<400> 2

cgcacgcgta	tgaaaatcat	tttcttcctc	tgttcatttc	tgttttttat	catcaatact	60
cagtgcgtga	cccacgaatc	ctatcaggag	ctgggttaaga	aactggaagc	tttggaagat	120
gccgtcctta	ccggatacag	cctgttccag	aaggagaaga	tggtgctgaa	tgaagggacg	180
agtggcacgg	ccgttacaac	cagcacaccc	ggttctaaag	ggtctgtggc	tagcgggtggc	240
tccggtgggt	ctgtggcctc	tgggggttcc	gtcgccctcg	gcggcagcgt	ggcatcaggt	300
ggctcagtgg	caagcggcgg	ttccgggaac	agtcgaagaa	ccaatccatc	tgacaactct	360
agcgattccg	acgccaagtc	ctacgccgac	ctcaagcacc	gagtgagaaa	ctatctcctc	420
actatcaagg	agctgaagta	cccacagttg	ttcgacctca	ctaatacatat	gctgacactg	480
tgtgataaca	ttcatggctt	caaatatctg	attgacgggt	acgaagagat	caatgaactc	540
ctgtacaagt	tgaattttcta	cttcgacttg	ctaagggccca	aactgaatga	cgtttgcgcc	600
aatgactatt	gtcaaatctc	attcaatttg	aagatcacag	ccaacgaggt	ggacgtattg	660
aagaagttgg	tcttcgggata	tcgcaagcct	ctcgacaaca	tcaaggacaa	tgtgggaaag	720
atggaagatt	atattaaaaa	gaataagaag	accatcgaga	acattaacga	gctgatcgaa	780
gaatccaaaa	agaccataga	caaaaataag	aatgcaacca	aggaggaaga	aaagaagaag	840
ttgtaccagg	cccagtagca	cctgtccatc	tataacaaac	agcttgaaga	agcccataac	900
ctcatcagcg	tactggagaa	gcgcatagac	accctcaaga	agaatgaaaa	tatcaaagaa	960
ctgctcgaca	agattaatga	aattaagaat	cctccgccag	ccaactctgg	gaacaccctc	1020
aacacgctgc	tggacaagaa	caagaagata	gaggagcacg	agaaagagat	caaagagatc	1080
gccaaaacca	ttaagttcaa	catagattct	ctctttactg	atccccttga	gctggagtag	1140
tacttgagag	agaagaataa	gaatatagac	atctccgccca	aagtcgagac	aaaggaatca	1200
accgaacctc	atgaatatcc	caatggtgtg	acgtaccctc	tgtcttataa	cgatatcaac	1260
aacgctctca	acgagctcaa	tagcttcggg	gacttgatta	accccttcga	ttatacgaaa	1320
gaaccctcta	agaatatcta	cacagacaat	gagagaaaga	agtttatcaa	cgaaatcaag	1380
gagaagatca	aaattgagaa	gaagaaaatt	gagagtgaac	agaaaagtta	cgaagaccgc	1440
agcaaaagtc	taaacgatat	cactaaagag	tatgaaaagc	tgctgaacga	gatctatgat	1500
tccaaattca	acaataacat	cgacctgacc	aacttcgaga	aaatgatggg	aaaacggtag	1560
tcttacaaag	tggagaaaact	gacacaccat	aatacctttg	catcctatga	gaattctaag	1620
cataatcttg	agaagctcac	caaagctctt	aagtatatgg	aggactattc	tctgcggaac	1680
attgttgtgg	agaaagaact	aaagtattac	aagaatctca	taagtaagat	cgaaaacgag	1740
atcgagacgc	ttgttgagaa	cattaagaag	gatgaagaac	agttgtttga	gaagaagatt	1800
acaaaagacg	aaaataaac	agatgagaag	atcctggagg	tctccgatat	tgttaaagtc	1860
caagtgcaga	aggtgtcctc	catgaacaag	attgatgaac	tcaagaagac	tcaactcatt	1920
ctgaagaacg	tggagttaaa	acataatata	catgtgccga	atagttataa	gcaggagaat	1980
aagcagggaac	catactacct	catcgtaact	aagaaagaga	tagacaaact	gaaagtgttc	2040
atgcccaaag	tcgagagcct	gatcaacgaa	gagaagaaga	acattaaaac	tgaaggacag	2100
tcagataact	ccgagccttc	cacagaagga	gagataaccg	gacaggctac	caccaagccc	2160
ggacaacagg	ccggttcagc	tctcgaaggc	gatagcgtgc	aagctcaagc	acaagagcag	2220
aagcaggcac	agcctccagt	gccagtgcc	gttcagagg	ctaaagctca	agtgcctaca	2280
ccaccagctc	ctgtgaataa	caagaccgag	aatgtcagca	aactggacta	ccttgagaag	2340
ctctatgagt	tctgaatac	atcctacatc	tgccacaaat	atatcctcgt	ctctcacagc	2400
actatgaacg	agaagattct	taaacagtac	aagataacca	aggaagagga	gagtaaactg	2460
tctcttgttg	atccactgga	cctgtgtgtc	aatatccaga	acaacattcc	cgttatgtat	2520
tctatgttcg	atagcctcaa	caattctctc	tctcaactgt	tcatggagat	atatgagaag	2580
gagatggtct	gcaacctgta	taaactcaaa	gacaacgaca	agattaagaa	ccttctggag	2640
gaagctaaga	aggtctccac	ctctgttaaa	actctctctt	ccagctccat	gcaaccactg	2700
tctctcacac	ctcaagacaa	gcccgaagtg	agcgctaacg	acgacacctc	tactcgacc	2760
aaccttaata	actcactgaa	actgtttgag	aacatcctgt	ctctcggcaa	gaataagaac	2820
atctaccaag	aacttattgg	acagaaatcg	tccgagaact	tctacgagaa	gatactgaaa	2880
gacagcgaca	cattctataa	cgagagcttc	actaacttcg	tgaaatctaa	agccgatgat	2940
atcaactctc	ttaacgatga	atctaaacgt	aagaagctgg	aagaggacat	caataagctg	3000
aagaagacac	tgcaactgag	cttcgacctg	tacaacaagt	acaaactgaa	actggagaga	3060

ctcttcgaca	agaagaagac	agtcggcaag	tataagatgc	agatcaagaa	gttgactctg	3120
ctcaaggagc	agcttgaaag	caaactcaac	tcactgaaca	atccgaaaca	cgtactgcag	3180
aacttctcag	tgttcttcaa	caagaagaag	gaagccgaga	tcgccgagac	agagaacact	3240
ctggagaaca	ccaagattct	tctcaaacac	tacaaaggcc	tcgtcaagta	ttataatggc	3300
gagtcttctc	ctctgaagac	tctctccgag	gagagcatcc	agaccgagga	taactacgcc	3360
agcctcgaga	acttcaaggt	cctgtctaag	ctcgaaggca	agctgaagga	caacctgaac	3420
ctggagaaga	agaagctcag	ctacctctct	agcggactgc	atcacctgat	cgccgagctc	3480
aaggaaagtca	ttaagaacaa	gaactacacc	ggcaatagcc	caagcgagaa	taatacacag	3540
gtgaataacg	cactggaatc	ttacaagaag	ttcctgcctg	aaggaaacaga	tgtcgccact	3600
gtggtgtctg	aatctggctc	cgacacactg	gagcagtctc	aacctaaaga	gcctgcatct	3660
actcatgtcg	gagccgagtc	caatacaatt	accacatctc	agaacgtcga	cgatgaggtc	3720
gatgacgtca	tcattgtgcc	tatcttcggc	gagagcgagg	aggactacga	tgacctcggc	3780
cagggtggtca	ccggtgaggc	tgctactcct	tccgtgattg	ataacattct	gtccaaaatc	3840
gagaacgaat	acgaagtgtc	ctatctgaaa	cctctggcag	gcgtctatag	gtctctcaag	3900
aaacagctgg	agaataacgt	gatgaccttc	aatgtcaacg	tgaaggacat	tctgaacagc	3960
cgctttaata	agagagaaaa	tttcaagaac	gtcttgagga	gcgacttgat	tccctataaa	4020
gacctgacct	cctctaacta	cgttgtcaag	gacccataca	agttcctcaa	taaagagaag	4080
agggataaat	ttctgtctag	ttacaactat	atcaaggact	ccatcgacac	cgatatcaat	4140
ttcgctaattg	atgtgtctggg	gtattacaag	atcctgagcg	aaaaatacaa	gtctgacctt	4200
gactctatta	aaaagtatat	caacgataag	caaggcgaga	atgaaaaata	tctgcccttc	4260
ctgaataaca	tcgaaaccct	gtacaagaca	gtgaacgaca	aaatcgacct	cttcgtaatt	4320
cacctggagg	ccaaggtcct	caactatact	tacgagaaga	gcaatgtgga	agttaaaatc	4380
aaggagctga	actacctcaa	aacaatccaa	gacaagctgg	cagatttcaa	gaaaaataac	4440
aatttcgctcg	gaattgcaga	cctgtctacc	gattataacc	acaacaatct	cctgaccaag	4500
tttctgtcca	ctggcatggg	gttcgaaaac	ctcgccaaaa	cagtgtctgag	caatctgctc	4560
gacggcaacc	tgcagggcac	gctgaacatc	tcccagcacc	aatgcgtgaa	gaaacagtg	4620
ccccagaata	gcggctgttt	caggcatctg	gacgagcgcg	aagagtgcaa	gtgtctcctg	4680
aactacaaaac	aagaaggaga	taagtgcgtg	gagaacccaa	accctacctg	caatgaaaac	4740
aatggcggggt	gtgacgcccga	tgctaaatgc	accgaggaag	acagcggtc	taacggaaag	4800
aaaatcacat	gcgagtgtac	taagcccgcac	tcctatccac	tcttcgacgg	gattttttgc	4860
tccagctcta	atttcctggg	catctccttc	ctgctgatcc	tcatgtctgat	cctgtacagc	4920
ttcatctaata	agatcgatgg					4940

<210> 3

<211> 1639

<212> PRT

<213> Plasmodium falciparum

<400> 3

Met	Lys	Ile	Ile	Phe	Phe	Leu	Cys	Ser	Phe	Leu	Phe	Phe	Ile	Ile	Asn
1				5					10					15	
Thr	Gln	Cys	Val	Thr	His	Glu	Ser	Tyr	Gln	Glu	Leu	Val	Lys	Lys	Leu
			20					25					30		
Glu	Ala	Leu	Glu	Asp	Ala	Val	Leu	Thr	Gly	Tyr	Ser	Leu	Phe	Gln	Lys
		35					40				45				
Glu	Lys	Met	Val	Leu	Asn	Glu	Gly	Thr	Ser	Gly	Thr	Ala	Val	Thr	Thr
	50					55					60				
Ser	Thr	Pro	Gly	Ser	Lys	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Gly	Gly
65					70				75					80	
Ser	Val	Ala	Ser	Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Val	Ala	Ser
				85				90						95	
Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Gly	Asn	Ser	Arg	Arg	Thr	Asn
		100						105					110		
Pro	Ser	Asp	Asn	Ser	Ser	Asp	Ser	Asp	Ala	Lys	Ser	Tyr	Ala	Asp	Leu
		115					120					125			
Lys	His	Arg	Val	Arg	Asn	Tyr	Leu	Leu	Thr	Ile	Lys	Glu	Leu	Lys	Tyr
	130					135					140				

Pro	Gln	Leu	Phe	Asp	Leu	Thr	Asn	His	Met	Leu	Thr	Leu	Cys	Asp	Asn
145					150					155					160
Ile	His	Gly	Phe	Lys	Tyr	Leu	Ile	Asp	Gly	Tyr	Glu	Glu	Ile	Asn	Glu
				165					170					175	
Leu	Leu	Tyr	Lys	Leu	Asn	Phe	Tyr	Phe	Asp	Leu	Leu	Arg	Ala	Lys	Leu
			180					185					190		
Asn	Asp	Val	Cys	Ala	Asn	Asp	Tyr	Cys	Gln	Ile	Pro	Phe	Asn	Leu	Lys
		195					200					205			
Ile	Arg	Ala	Asn	Glu	Leu	Asp	Val	Leu	Lys	Lys	Leu	Val	Phe	Gly	Tyr
	210					215					220				
Arg	Lys	Pro	Leu	Asp	Asn	Ile	Lys	Asp	Asn	Val	Gly	Lys	Met	Glu	Asp
225					230					235				240	
Tyr	Ile	Lys	Lys	Asn	Lys	Lys	Thr	Ile	Glu	Asn	Ile	Asn	Glu	Leu	Ile
				245					250					255	
Glu	Glu	Ser	Lys	Lys	Thr	Ile	Asp	Lys	Asn	Lys	Asn	Ala	Thr	Lys	Glu
			260					265					270		
Glu	Glu	Lys	Lys	Lys	Leu	Tyr	Gln	Ala	Gln	Tyr	Asp	Leu	Ser	Ile	Tyr
		275					280					285			
Asn	Lys	Gln	Leu	Glu	Glu	Ala	His	Asn	Leu	Ile	Ser	Val	Leu	Glu	Lys
	290					295					300				
Arg	Ile	Asp	Thr	Leu	Lys	Lys	Asn	Glu	Asn	Ile	Lys	Glu	Leu	Leu	Asp
305					310					315					320
Lys	Ile	Asn	Glu	Ile	Lys	Asn	Pro	Pro	Pro	Ala	Asn	Ser	Gly	Asn	Thr
				325					330					335	
Pro	Asn	Thr	Leu	Leu	Asp	Lys	Asn	Lys	Lys	Ile	Glu	Glu	His	Glu	Lys
			340					345					350		
Glu	Ile	Lys	Glu	Ile	Ala	Lys	Thr	Ile	Lys	Phe	Asn	Ile	Asp	Ser	Leu
		355					360					365			
Phe	Thr	Asp	Pro	Leu	Glu	Leu	Glu	Tyr	Tyr	Leu	Arg	Glu	Lys	Asn	Lys
	370					375					380				
Asn	Ile	Asp	Ile	Ser	Ala	Lys	Val	Glu	Thr	Lys	Glu	Ser	Thr	Glu	Pro
385					390					395					400
Asn	Glu	Tyr	Pro	Asn	Gly	Val	Thr	Tyr	Pro	Leu	Ser	Tyr	Asn	Asp	Ile
				405					410					415	
Asn	Asn	Ala	Leu	Asn	Glu	Leu	Asn	Ser	Phe	Gly	Asp	Leu	Ile	Asn	Pro
			420					425					430		
Phe	Asp	Tyr	Thr	Lys	Glu	Pro	Ser	Lys	Asn	Ile	Tyr	Thr	Asp	Asn	Glu
		435					440					445			
Arg	Lys	Lys	Phe	Ile	Asn	Glu	Ile	Lys	Glu	Lys	Ile	Lys	Ile	Glu	Lys
	450					455					460				
Lys	Lys	Ile	Glu	Ser	Asp	Lys	Lys	Ser	Tyr	Glu	Asp	Arg	Ser	Lys	Ser
465					470					475					480
Leu	Asn	Asp	Ile	Thr	Lys	Glu	Tyr	Glu	Lys	Leu	Leu	Asn	Glu	Ile	Tyr
				485					490					495	
Asp	Ser	Lys	Phe	Asn	Asn	Asn	Ile	Asp	Leu	Thr	Asn	Phe	Glu	Lys	Met
			500					505					510		
Met	Gly	Lys	Arg	Tyr	Ser	Tyr	Lys	Val	Glu	Lys	Leu	Thr	His	His	Asn
		515					520					525			
Thr	Phe	Ala	Ser	Tyr	Glu	Asn	Ser	Lys	His	Asn	Leu	Glu	Lys	Leu	Thr
		530				535					540				
Lys	Ala	Leu	Lys	Tyr	Met	Glu	Asp	Tyr	Ser	Leu	Arg	Asn	Ile	Val	Val
545					550					555					560
Glu	Lys	Glu	Leu	Lys	Tyr	Tyr	Lys	Asn	Leu	Ile	Ser	Lys	Ile	Glu	Asn
				565					570					575	
Glu	Ile	Glu	Thr	Leu	Val	Glu	Asn	Ile	Lys	Lys	Asp	Glu	Glu	Gln	Leu
			580					585					590		
Phe	Glu	Lys	Lys	Ile	Thr	Lys	Asp	Glu	Asn	Lys	Pro	Asp	Glu	Lys	Ile

Gln Asn Phe Ser Val Phe Phe Asn Lys Lys Lys Glu Ala Glu Ile Ala
 1060 1065 1070
 Glu Thr Glu Asn Thr Leu Glu Asn Thr Lys Ile Leu Leu Lys His Tyr
 1075 1080 1085
 Lys Gly Leu Val Lys Tyr Tyr Asn Gly Glu Ser Ser Pro Leu Lys Thr
 1090 1095 1100
 Leu Ser Glu Glu Ser Ile Gln Thr Glu Asp Asn Tyr Ala Ser Leu Glu
 1105 1110 1115 1120
 Asn Phe Lys Val Leu Ser Lys Leu Glu Gly Lys Leu Lys Asp Asn Leu
 1125 1130 1135
 Asn Leu Glu Lys Lys Lys Leu Ser Tyr Leu Ser Ser Gly Leu His His
 1140 1145 1150
 Leu Ile Ala Glu Leu Lys Glu Val Ile Lys Asn Lys Asn Tyr Thr Gly
 1155 1160 1165
 Asn Ser Pro Ser Glu Asn Asn Thr Asp Val Asn Asn Ala Leu Glu Ser
 1170 1175 1180
 Tyr Lys Lys Phe Leu Pro Glu Gly Thr Asp Val Ala Thr Val Val Ser
 1185 1190 1195 1200
 Glu Ser Gly Ser Asp Thr Leu Glu Gln Ser Gln Pro Lys Lys Pro Ala
 1205 1210 1215
 Ser Thr His Val Gly Ala Glu Ser Asn Thr Ile Thr Thr Ser Gln Asn
 1220 1225 1230
 Val Asp Asp Glu Val Asp Asp Val Ile Ile Val Pro Ile Phe Gly Glu
 1235 1240 1245
 Ser Glu Glu Asp Tyr Asp Asp Leu Gly Gln Val Val Thr Gly Glu Ala
 1250 1255 1260
 Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu
 1265 1270 1275 1280
 Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu
 1285 1290 1295
 Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys
 1300 1305 1310
 Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val
 1315 1320 1325
 Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr
 1330 1335 1340
 Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys
 1345 1350 1355 1360
 Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile
 1365 1370 1375
 Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys
 1380 1385 1390
 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln
 1395 1400 1405
 Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr Leu
 1410 1415 1420
 Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu
 1425 1430 1435 1440
 Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys
 1445 1450 1455
 Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp
 1460 1465 1470
 Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp
 1475 1480 1485
 Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val
 1490 1495 1500
 Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn

1505		1510		1515		1520
Leu Gln Gly Met	Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln					
	1525		1530		1535	
Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu						
	1540		1545		1550	
Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu						
	1555		1560		1565	
Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp						
	1570		1575		1580	
Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr						
1585		1590		1595		1600
Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe						
	1605		1610		1615	
Cys Ser Ser Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met						
	1620		1625		1630	
Leu Ile Leu Tyr Ser Phe Ile						
	1635					

<210> 4

<211> 4894

<212> DNA

<213> Plasmodium falciparum

<400> 4

gcacgcgtat	gaaaatcatt	ttcttcctct	gttcatttct	gtttttttatc	atcaatactc	60
agtgcgtgac	ccacgaatcc	tatcaggagc	tggttaagaa	actggaagct	ttggaagatg	120
ccgtccttac	cggatacagc	ctgttccaga	aggagaagat	ggtgctgaat	gaagggacga	180
gtggcacggc	cgttacaacc	agcacacccg	gttctaaagg	gtctgtggct	agcgggtggct	240
ccgggtgggtc	tgtggcctct	gggggttccg	tcgcctccgg	cggcagcgtg	gcatcagggtg	300
gctcagtggc	aagcggcggg	tccgggaaca	gtcgaagaac	caatccatct	gacaactcta	360
gcgattccga	cgccaagtcc	tacgccgacc	tcaagcaccg	agtgagaaac	tatctcctca	420
ctatcaagga	gctgaagtac	ccacagttgt	tcgacctcac	taatcatatg	ctgacactgt	480
gtgataacat	tcatggcttc	aaatatctga	ttgacgggta	cgaagagatc	aatgaactcc	540
tgtacaagtt	gaatttctac	ttcgacttgc	taagggccaa	actgaatgac	gtttgcgcca	600
atgactattg	tcaaattcca	ttcaatttga	agatcagagc	caacgagttg	gacgtattga	660
agaagttggt	cttcggatat	cgcaagcctc	tcgacaacat	caaggacaat	gtgggaaaga	720
tggaaagatta	tattaaaaag	aataagaaga	ccatcgagaa	cattaacgag	ctgatcgaag	780
aatccaaaaa	gaccatagac	aaaaataaga	atgcaaccaa	ggaggaagaa	aagaagaagt	840
tgtaccaggc	ccagtagcac	ctgtccatct	ataacaaaca	gcttgaagaa	gcccataaacc	900
tcatcagcgt	actggagaag	cgcatagaca	ccctcaagaa	gaatgaaaat	atcaaagaac	960
tgctcgacaa	gattaatgaa	attaagaatc	ctccgccagc	caactctggg	aacaccctta	1020
acacgctgct	ggacaagaac	aagaagatag	aggagcacga	gaaagagatc	aaagagatcg	1080
ccaaaaccat	taagttcaac	atagattctc	tctttactga	tccccttgag	ctggagtact	1140
acttgagaga	gaagaataag	aatatagaca	tctccgccaa	agtcgagaca	aaggaatcaa	1200
ccgaacctaa	tgaatatccc	aatggtgtga	cgtaccctct	gtcttataac	gatatacaaca	1260
acgctctcaa	cgagctcaat	agcttcgggtg	acttgattaa	ccccttcgat	tatacgaaag	1320
aaccctctaa	gaatatctac	acagacaatg	agagaaagaa	gtttatcaac	gaaatcaagg	1380
agaagatcaa	aattgagaag	aagaaaattg	agagtgaaca	gaaaagttac	gaagaccgca	1440
gcaaaagtct	aaacgatatc	actaaagagt	atgaaaagct	gctgaacgag	atctatgatt	1500
ccaaattcaa	caataacatc	gacctgacca	acttcgagaa	aatgatggga	aaacggtact	1560
cttacaaagt	ggagaaactg	acacaccata	atacctttgc	atcctatgag	aattctaagc	1620
ataatcttga	gaagctcacc	aaagctctta	agtatatgga	ggactattct	ctgcggaaca	1680
ttgttggtgga	gaaagaacta	aagtattaca	agaatctcat	aagtaagatc	gaaaacgaga	1740
tcgagacgct	tgttgagaac	attaagaagg	atgaagaaca	gttgtttgag	aagaagatta	1800
caaaagacga	aaataaacca	gatgagaaga	tcctggagggt	ctccgatatt	gttaaagtcc	1860
aagtgcagaa	ggtgctcctc	atgaacaaga	ttgatgaact	caagaagact	caactcattc	1920
tgaagaacgt	ggagttaaaa	cataatatac	atgtgcccga	tagttataag	caggagaata	1980

agcaggaacc	atactacctc	atcgtactca	agaaagagat	agacaaactg	aaagtgttca	2040
tgcccaaagt	cgagagcctg	atcaacgaag	agaagaagaa	cattaaaact	gaaggacagt	2100
cagataactc	cgagccttcc	acagaaggag	agataaccgg	acaggctacc	accaagcccg	2160
gacaacaggc	cggttcagct	ctcgaaggcg	atagcgtgca	agctcaagca	caagagcaga	2220
agcaggcaca	gcctccagtg	ccagtgcccc	ttccagaggc	taaagctcaa	gtgcctacac	2280
caccagctcc	tgtgaataac	aagaccgaga	atgtcagcaa	actggactac	cttgagaagc	2340
tctatgagtt	cctgaatata	tcctacatct	gccacaaata	tatcctcgtc	tctcacagca	2400
ctatgaacga	gaagattcct	aaacagtaca	agataaccaa	ggaagaggag	agtaaactgt	2460
cctcttgtga	tccactggac	ctgctgttca	atatccagaa	caacattccc	gttatgtatt	2520
ctatgttcga	tagcctcaac	aattctctct	ctcaactggt	catggagata	tatgagaagg	2580
agatggtctg	caacctgtat	aaactcaaa	acaacgacaa	gattaagaac	cttctggagg	2640
aagctaagaa	ggtctccacc	tctgttaaaa	ctctctcttc	cagctccatg	caaccactgt	2700
ctctcacacc	tcaagacaag	cccgaagtga	gcgctaacga	cgacacctct	cactcgacca	2760
accttaataa	ctcactgaaa	ctgtttgaga	acatcctgtc	tctcggcaag	aataagaaca	2820
tctaccaaga	acttattgga	cagaaatcgt	ccgagaactt	ctacgagaag	atactgaaag	2880
acagcgacac	attctataac	gagagcttca	ctaacttcgt	gaaatctaaa	gccgatgata	2940
tcaactctct	taacgatgaa	tctaaacgta	agaagctgga	agaggacatc	aataagctga	3000
agaagacact	gcaactgagc	ttcgacctgt	acaacaagta	caaactgaaa	ctggagagac	3060
tcttcgacaa	gaagaagaca	gtcggcaagt	ataagatgca	gatcaagaag	ttgactctgc	3120
tcaaggagca	gcttgaaagc	aaactcaact	cactgaacaa	tccgaaacac	gtactgcaga	3180
acttctcagt	gttcttcaac	aagaagaagg	aagccgagat	cgccgagaca	gagaacactc	3240
tggagaacac	caagattctt	ctcaaact	acaaaggcct	cgtcaagtat	tataatggcg	3300
agtcttctcc	tctgaagact	ctctccgagg	agagcatcca	gaccgaggat	aactacgcca	3360
gcctcgagaa	cttcaaggtc	ctgtctaagc	togaaggcaa	gctgaaggac	aacctgaacc	3420
tggagaagaa	gaagctcagc	tacctctcta	gcggaactgca	tcacctgate	gccgagctca	3480
aggaagtcat	taagaacaag	aactacaccg	gcaatagccc	aagcgagaat	aatacagacg	3540
tgaataacgc	actggaatct	tacaagaagt	tccctgctga	aggaacagat	gtcggccactg	3600
tgggtgtctga	acttggtctc	gacacactgg	agcagctctca	acctagaag	cctgcactcta	3660
ctcatgtcgg	agccgagtc	aatacaatta	ccacatctca	gaacgtcgac	gatgaggtcg	3720
atgacgtcat	cattgtgcct	atcttcggcg	agagcgagga	ggactacgat	gacctcggcc	3780
aggtggtcac	cggtagaggct	gtcactcctt	ccgtgattga	taacattctg	tccaaaatcg	3840
agaacgaata	cgaagtgtc	tatctgaaac	ctctggcagg	cgtctatagg	tctctcaaga	3900
aacagctgga	gaataacgtg	atgaccttca	atgtcaacgt	gaaggacatt	ctgaacagcc	3960
gctttaataa	gagagaaaat	ttcaagaacg	tcttgagag	cgacttgatt	ccctataaag	4020
acctgacctc	ctctaactac	gttgtcaagg	acccatacaa	gttcctcaat	aaagagaaga	4080
gggataaatt	tctgtctagt	tacaactata	tcaaggactc	catcgacacc	gatatcaatt	4140
tcgctaattga	tgtgctgggg	tattacaaga	tccctgagcga	aaaataacaag	tctgaccttg	4200
actctattaa	aaagtatatc	aacgataagc	aaggcgagaa	tgaaaaatat	ctgcccttcc	4260
tgaataacat	cgaaacctctg	tacaagacag	tgaacgacaa	aatcgacctc	ttcgtaattc	4320
acctggaggc	caaggctctc	aactatactt	acgagaagag	caatgtggaa	gttaaaatca	4380
aggagctgaa	ctacctcaaa	acaatccaag	acaagctggc	agatttcaag	aaaaataaca	4440
atttcgtcgg	aattgcagac	ctgtctaccg	attataacca	caacaatctc	ctgaccaagt	4500
ttctgtccac	tggcatggtg	ttcgaaaacc	tcgccaaaac	agtgtgagc	aatctgctcg	4560
acggcaacct	gcagggcatg	ctgaacatct	cccagcacca	atgcgtgaag	aaacagtgcc	4620
cccagaatag	cggctgtttc	aggcatctgg	acgagcgcg	agagtgcag	tgtctcctga	4680
actacaaaca	agaaggagat	aagtgcgtgg	agaacccaaa	ccctacctgc	aatgaaaaca	4740
atggcgggtg	tgacgccgat	gctaaatgca	ccgagggaaga	cagcggctct	aacgggaaaga	4800
aatcacatg	cgagtgtact	aagcccagct	cctatccact	cttcgacggg	atTTTTTgct	4860
ccagctctaa	ttaataggcg	gccgcatcga	tggc			4894

<210> 5

<211> 1621

<212> PRT

<213> Plasmodium falciparum

<400> 5

Met Lys Ile Ile Phe Phe Leu Cys Ser Phe Leu Phe Phe Ile Ile Asn

1				5				10					15			
Thr	Gln	Cys	Val	Thr	His	Glu	Ser	Tyr	Gln	Glu	Leu	Val	Lys	Lys	Leu	
			20					25					30			
Glu	Ala	Leu	Glu	Asp	Ala	Val	Leu	Thr	Gly	Tyr	Ser	Leu	Phe	Gln	Lys	
	35						40					45				
Glu	Lys	Met	Val	Leu	Asn	Glu	Gly	Thr	Ser	Gly	Thr	Ala	Val	Thr	Thr	
	50					55					60					
Ser	Thr	Pro	Gly	Ser	Lys	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Gly	Gly	
65					70					75					80	
Ser	Val	Ala	Ser	Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Val	Ala	Ser	
			85					90						95		
Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Gly	Asn	Ser	Arg	Arg	Thr	Asn	
			100					105					110			
Pro	Ser	Asp	Asn	Ser	Ser	Asp	Ser	Asp	Ala	Lys	Ser	Tyr	Ala	Asp	Leu	
	115						120					125				
Lys	His	Arg	Val	Arg	Asn	Tyr	Leu	Leu	Thr	Ile	Lys	Glu	Leu	Lys	Tyr	
	130					135					140					
Pro	Gln	Leu	Phe	Asp	Leu	Thr	Asn	His	Met	Leu	Thr	Leu	Cys	Asp	Asn	
145					150					155					160	
Ile	His	Gly	Phe	Lys	Tyr	Leu	Ile	Asp	Gly	Tyr	Glu	Glu	Ile	Asn	Glu	
			165					170						175		
Leu	Leu	Tyr	Lys	Leu	Asn	Phe	Tyr	Phe	Asp	Leu	Leu	Arg	Ala	Lys	Leu	
			180					185					190			
Asn	Asp	Val	Cys	Ala	Asn	Asp	Tyr	Cys	Gln	Ile	Pro	Phe	Asn	Leu	Lys	
	195						200					205				
Ile	Arg	Ala	Asn	Glu	Leu	Asp	Val	Leu	Lys	Lys	Leu	Val	Phe	Gly	Tyr	
	210					215					220					
Arg	Lys	Pro	Leu	Asp	Asn	Ile	Lys	Asp	Asn	Val	Gly	Lys	Met	Glu	Asp	
225					230					235				240		
Tyr	Ile	Lys	Lys	Asn	Lys	Lys	Thr	Ile	Glu	Asn	Ile	Asn	Glu	Leu	Ile	
			245						250				255			
Glu	Glu	Ser	Lys	Lys	Thr	Ile	Asp	Lys	Asn	Lys	Asn	Ala	Thr	Lys	Glu	
			260					265					270			
Glu	Glu	Lys	Lys	Lys	Leu	Tyr	Gln	Ala	Gln	Tyr	Asp	Leu	Ser	Ile	Tyr	
	275						280					285				
Asn	Lys	Gln	Leu	Glu	Glu	Ala	His	Asn	Leu	Ile	Ser	Val	Leu	Glu	Lys	
	290					295					300					
Arg	Ile	Asp	Thr	Leu	Lys	Lys	Asn	Glu	Asn	Ile	Lys	Glu	Leu	Leu	Asp	
305					310					315					320	
Lys	Ile	Asn	Glu	Ile	Lys	Asn	Pro	Pro	Pro	Ala	Asn	Ser	Gly	Asn	Thr	
			325					330					335			
Pro	Asn	Thr	Leu	Leu	Asp	Lys	Asn	Lys	Lys	Ile	Glu	Glu	His	Glu	Lys	
	340							345					350			
Glu	Ile	Lys	Glu	Ile	Ala	Lys	Thr	Ile	Lys	Phe	Asn	Ile	Asp	Ser	Leu	
	355						360					365				
Phe	Thr	Asp	Pro	Leu	Glu	Leu	Glu	Tyr	Tyr	Leu	Arg	Glu	Lys	Asn	Lys	
	370					375				380						
Asn	Ile	Asp	Ile	Ser	Ala	Lys	Val	Glu	Thr	Lys	Glu	Ser	Thr	Glu	Pro	
385					390					395					400	
Asn	Glu	Tyr	Pro	Asn	Gly	Val	Thr	Tyr	Pro	Leu	Ser	Tyr	Asn	Asp	Ile	
			405						410					415		
Asn	Asn	Ala	Leu	Asn	Glu	Leu	Asn	Ser	Phe	Gly	Asp	Leu	Ile	Asn	Pro	
	420							425					430			
Phe	Asp	Tyr	Thr	Lys	Glu	Pro	Ser	Lys	Asn	Ile	Tyr	Thr	Asp	Asn	Glu	
	435						440					445				
Arg	Lys	Lys	Phe	Ile	Asn	Glu	Ile	Lys	Glu	Lys	Ile	Lys	Ile	Glu	Lys	
	450					455					460					

Lys 465	Lys	Ile	Glu	Ser	Asp 470	Lys	Lys	Ser	Tyr	Glu 475	Asp	Arg	Ser	Lys	Ser 480
Leu	Asn	Asp	Ile	Thr	Lys 485	Glu	Tyr	Glu	Lys 490	Leu	Leu	Asn	Glu	Ile	Tyr 495
Asp	Ser	Lys	Phe	Asn	Asn	Asn	Ile	Asp 500	Leu	Thr	Asn	Phe	Glu	Lys	Met 510
Met	Gly	Lys	Arg	Tyr	Ser	Tyr	Lys	Val 515	Glu	Lys	Leu	Thr	His	His	Asn 525
Thr	Phe	Ala	Ser	Tyr	Glu	Asn	Ser	Lys 530	His	Asn	Leu	Glu	Lys	Leu	Thr 540
Lys 545	Ala	Leu	Lys	Tyr	Met	Glu	Asp	Tyr	Ser	Leu	Arg	Asn	Ile	Val	Val 560
Glu	Lys	Glu	Leu	Lys	Tyr	Tyr	Lys	Asn	Leu	Ile	Ser	Lys	Ile	Glu	Asn 575
Glu	Ile	Glu	Thr	Leu	Val	Glu	Asn	Ile	Lys	Lys	Asp	Glu	Glu	Gln	Leu 590
Phe	Glu	Lys	Lys	Ile	Thr	Lys	Asp	Glu	Asn	Lys	Pro	Asp	Glu	Lys	Ile 605
Leu	Glu	Val	Ser	Asp	Ile	Val	Lys	Val	Gln	Val	Gln	Lys	Val	Leu	Leu 620
Met 625	Asn	Lys	Ile	Asp	Glu	Leu	Lys	Lys	Thr	Gln	Leu	Ile	Leu	Lys	Asn 640
Val	Glu	Leu	Lys	His	Asn	Ile	His	Val	Pro	Asn	Ser	Tyr	Lys	Gln	Glu 655
Asn	Lys	Gln	Glu	Pro	Tyr	Tyr	Leu	Ile	Val	Leu	Lys	Lys	Glu	Ile	Asp 670
Lys	Leu	Lys	Val	Phe	Met	Pro	Lys	Val	Glu	Ser	Leu	Ile	Asn	Glu	Glu 685
Lys 690	Lys	Asn	Ile	Lys	Thr	Glu	Gly	Gln	Ser	Asp	Asn	Ser	Glu	Pro	Ser 700
Thr 705	Glu	Gly	Glu	Ile	Thr	Gly	Gln	Ala	Thr	Thr	Lys	Pro	Gly	Gln	Gln 720
Ala	Gly	Ser	Ala	Leu	Glu	Gly	Asp	Ser	Val	Gln	Ala	Gln	Ala	Gln	Glu 735
Gln	Lys	Gln	Ala	Gln	Pro	Pro	Val	Pro	Val	Pro	Val	Pro	Glu	Ala	Lys 750
Ala	Gln	Val	Pro	Thr	Pro	Pro	Ala	Pro	Val	Asn	Asn	Lys	Thr	Glu	Asn 765
Val	Ser	Lys	Leu	Asp	Tyr	Leu	Glu	Lys	Leu	Tyr	Glu	Phe	Leu	Asn	Thr 780
Ser 785	Tyr	Ile	Cys	His	Lys	Tyr	Ile	Leu	Val	Ser	His	Ser	Thr	Met	Asn 800
Glu	Lys	Ile	Leu	Lys	Gln	Tyr	Lys	Ile	Thr	Lys	Glu	Glu	Glu	Ser	Lys 815
Leu	Ser	Ser	Cys	Asp	Pro	Leu	Asp	Leu	Leu	Phe	Asn	Ile	Gln	Asn	Asn 830
Ile	Pro	Val	Met	Tyr	Ser	Met	Phe	Asp	Ser	Leu	Asn	Asn	Ser	Leu	Ser 845
Gln	Leu	Phe	Met	Glu	Ile	Tyr	Glu	Lys	Glu	Met	Val	Cys	Asn	Leu	Tyr 860
Lys 865	Leu	Lys	Asp	Asn	Asp	Lys	Ile	Lys	Asn	Leu	Leu	Glu	Glu	Ala	Lys 880
Lys	Val	Ser	Thr	Ser	Val	Lys	Thr	Leu	Ser	Ser	Ser	Ser	Met	Gln	Pro 895
Leu	Ser	Leu	Thr	Pro	Gln	Asp	Lys	Pro	Glu	Val	Ser	Ala	Asn	Asp	Asp 910
Thr	Ser	His	Ser	Thr	Asn	Leu	Asn	Asn	Ser	Leu	Lys	Leu	Phe	Glu	Asn

Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys
 1380 1385 1390
 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln
 1395 1400 1405
 Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr Leu
 1410 1415 1420
 Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu
 1425 1430 1435 1440
 Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys
 1445 1450 1455
 Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp
 1460 1465 1470
 Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp
 1475 1480 1485
 Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val
 1490 1495 1500
 Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn
 1505 1510 1515 1520
 Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln
 1525 1530 1535
 Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu
 1540 1545 1550
 Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu
 1555 1560 1565
 Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp
 1570 1575 1580
 Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr
 1585 1590 1595 1600
 Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe
 1605 1610 1615
 Cys Ser Ser Ser Asn
 1620

<210> 6
 <211> 4838
 <212> DNA
 <213> Plasmodium falciparum

<400> 6
 gcggatccgt gaccacgaa tcctatcagg agctgggttaa gaaactggaa gcttttgaag 60
 atgccgtcct taccggatac agcctgttcc agaaggagaa gatggtgctg aatgaaggga 120
 cgagtggcac ggccgttaca accagcacac ccggttctaa agggctctgtg gctagcgggtg 180
 gctccggtgg gtctgtggcc tctgggggtt cctgcgcctc cggcggcagc gtggcatcag 240
 gtggctcagt ggcaagcggc gggtccggga acagtcgaag aaccaatcca tctgacaact 300
 ctagcgattc cgacgccaag tcctacgccg acctcaagca ccgagtgaga aactatctcc 360
 tcactatcaa ggagctgaag taccacacagt tggttcgacct cactaatcat atgctgacac 420
 tgtgtgataa cattcatggc ttcaaatac tgattgacgg ttacgaagag atcaatgaac 480
 tcctgtacaa gttgaatttc tacttcgact tgctaagggc caaactgaat gacgtttgcg 540
 ccaatgacta ttgtcaaatt ccattcaatt tgaagatcag agccaacgag ttggacgtat 600
 tgaagaagtt ggtcttcgga tatcgcaagc ctctcgacaa catcaaggac aatgtgggaa 660
 agatggaaga ttatattaaa aagaataaga agaccatcga gaacattaac gagctgatcg 720
 aagaatccaa aaagaccata gacaaaaata agaatgcaac caaggaggaa gaaaagaaga 780
 agttgtacca ggcccagtac gacctgtcca tctataacaa acagcttgaa gaagcccata 840
 acctcatcag cgtactggag aagcgcatag acaccctcaa gaagaatgaa aatatcaaag 900
 aactgctcga caagattaat gaaattaaga atcctccgcc agccaactct gggaacaccc 960
 ctaacacgct gctggacaag aacaagaaga tagaggagca cgagaaagag atcaaagaga 1020
 tcgccaaaac cattaagttc aacatagatt ctctctttac tgatcccctt gagctggagt 1080

actacttgag	agagaagaat	aagaatatag	acatctccgc	caaagtcgag	acaaaggaat	1140
caaccgaacc	taatgaatat	cccaatggtg	tgacgtaccc	tctgtcttat	aacgatatca	1200
acaacgctct	caacgagctc	aatagcttcg	gtgacttgat	taacccttc	gattatacga	1260
aagaaccctc	taagaatatc	tacacagaca	atgagagaaa	gaagtttatc	aacgaaatca	1320
aggagaagat	caaaattgag	aagaagaaaa	ttgagagtga	caagaaaagt	tacgaagacc	1380
gcagcaaaaag	tctaaacgat	atcactaaag	agtatgaaaa	gctgctgaac	gagatctatg	1440
attccaaatt	caacaataac	atcgacctga	ccaacttcga	gaaaatgatg	ggaaaacggt	1500
actcttacia	agtggagaaa	ctgacacacc	ataatacctt	tgcatcctat	gagaattcta	1560
agcataatct	tgagaagctc	accaaagctc	ttaagtatat	ggaggactat	tctctgcgga	1620
acattgttgt	ggagaaagaa	ctaaagtatt	acaagaatct	cataagtaag	atcgaaaacg	1680
agatcgagac	gcttggtgag	aacattaaga	aggatgaaga	acagttgttt	gagaagaaga	1740
ttacaaaaga	cgaaaataaa	ccagatgaga	agatcctgga	ggtctccgat	attgttaaag	1800
tccaagtgca	gaaggtgctc	ctcatgaaca	agattgatga	actcaagaag	actcaactca	1860
ttctgaagaa	cgtggaggtta	aaacataata	tacatgtgcc	gaatagttat	aagcaggaga	1920
ataagcagga	accatactac	ctcatcgta	tcaagaaaga	gatagacaaa	ctgaaagtgt	1980
tcatgcccaa	agtcgagagc	ctgatcaacg	aagagaagaa	gaacattaaa	actgaaggac	2040
agtcagataa	tcccgagcct	tccacagaag	gagagataac	cggacaggct	accaccaagc	2100
ccggacaaca	ggccggttca	gctctcgaag	cgcgatagcgt	gcaagctcaa	gcacaagagc	2160
agaagcaggc	acagcctcca	gtgccagtgc	cggttccaga	ggctaaagct	caagtgccta	2220
caccaccagc	tctgtgta	aacaagaccg	agaatgtcag	caaactggac	taccttgaga	2280
agctctatga	gttcttga	acatcctaca	tctgccacaa	atatactctc	gtctctcaca	2340
gcactatgaa	cgagaagatt	cttaaacagt	acaagataac	caaggaagag	gagagtaa	2400
tgctctcttg	tgatccactg	gacctgctgt	tcaatatcca	gaacaacatt	cccgttatgt	2460
attctatggt	cgatagcctc	aacaattctc	tctctcaact	gttcatggag	atataatgaga	2520
aggagatggt	ctgcaacctg	tataaactca	aagacaacga	caagattaag	aaccttctgg	2580
aggaagctaa	gaaggtctcc	acctctgtta	aaactctctc	ttccagctcc	atgcaaccac	2640
tgctctctac	acctcaagac	aagcccgaag	tgagcgctaa	cgacgacacc	tctcactcga	2700
ccaaccttaa	taactcactg	aaactgtttg	agaacatcct	gtctctcggc	aagaataaga	2760
acatctacca	agaacttatt	ggacagaaat	cgtccgagaa	cttctacgag	aagatactga	2820
aagacagcga	cacattctat	aacgagagct	tacttaactt	cgtgaaatct	aaagccgatg	2880
atatcaactc	tcttaacgat	gaatctaaac	gtaagaagct	ggaagaggac	atcaataagc	2940
tgaagaagac	actgcaactg	agcttcgacc	tgtacaacaa	gtacaaactg	aaactggaga	3000
gactcttcga	caagaagaag	acagtcggca	agtataagat	gcagatcaag	aagttgactc	3060
tgctcaagga	gcagcttgaa	agcaaactca	actcactgaa	caatccgaaa	cacgtactgc	3120
agaacttctc	agtgttcttc	aacaagaaga	aggaagccga	gatcgccgag	acagagaaca	3180
ctctggagaa	caccaagatt	cttctcaa	actacaaagg	cctcgtcaag	tattataatg	3240
gcgagctctc	tctctgaag	actctctccg	aggagagcat	ccagaccgag	gataactacg	3300
ccagcctcga	gaacttcaag	gtcctgtcta	agctcgaagg	caagctgaag	gacaacctga	3360
acctggagaa	gaagaagctc	agctacctct	ctagcggact	gcatcacctg	atcgccgagc	3420
tcaagggaag	cattaagaac	aagaactaca	ccggcaatag	cccaagcgag	aataatacag	3480
acgtgaataa	cgcactggaa	tcttacaaga	agttcctgcc	tgaaggaa	gatgtcgcca	3540
ctgtggtgtc	tgaatctggc	tccgacacac	tggagcagtc	tcaacctaa	aagcctgcat	3600
ctactcatgt	cggagccgag	tccaatacaa	ttaccacatc	tcagaacgtc	gacgatgagg	3660
tcatgacgt	catcattgtg	cctatcttcg	gcgagagcga	ggaggactac	gatgacctcg	3720
gccaggtggt	caccggtgag	gctgtcactc	cttccgtgat	tgataacatt	ctgtccaaaa	3780
tcgagaacga	atacgaagtg	ctctatctga	aacctctggc	aggcgtctat	aggtctctca	3840
agaaacagct	ggagaataac	gtgatgacct	tcaatgtcaa	cgtgaaggac	attctgaaca	3900
gccgctttaa	taagagagaa	aatttcaaga	acgtcttggg	gagcgacttg	attccctata	3960
aagacctgac	ctcctcta	tacgttgtca	aggaccata	caagttcctc	aataaagaga	4020
agagggataa	atttctgtct	agttacaact	atatcaagga	ctccatcgac	accgatatca	4080
atttcgctaa	tgatgtgctg	gggtattaca	agatcctgag	cgaaaaatac	aagtctgacc	4140
ttgactctat	taaaaagtat	atcaacgata	agcaaggcga	gaatgaaaaa	tatctgccct	4200
tctgaataa	catcgaaacc	ctgtacaaga	cagtgaacga	caaaatcgac	ctcttcgtaa	4260
ttcacctgga	ggccaaggtc	ctcaactata	cttacgagaa	gagcaatgtg	gaagttaaaa	4320
tcaaggagct	gaactacctc	aaaacaatcc	aagacaagct	ggcagatttc	aagaaaaata	4380
acaatttcgt	cgggaattgca	gacctgtcta	ccgattataa	ccacaacaat	ctcctgacca	4440
agtttctgtc	cactggcagtg	gtgttcgaaa	acctcgccaa	aacagtgtctg	agcaatctgc	4500

tcgacggcaa	cctgcagggc	atgctgaaca	tctcccagca	ccaatgcgtg	aagaaacagt	4560
gccccagaa	tagcggctgt	ttcaggcatc	tggacgagcg	cgaagagtgc	aagtgtctcc	4620
tgaactacaa	acaagaagga	gataagtgcg	tggagaaccc	aaaccctacc	tgcaatgaaa	4680
acaatggcgg	gtgtgacgcc	gatgctaaat	gcaccgagga	agacagcggc	tctaacggaa	4740
agaaaatcac	atgcgagtgt	actaagcccc	actcctatcc	actcttcgac	gggatttttt	4800
gctccagctc	taatttaata	ggcggccgca	tcgatggc			4838

<210> 7

<211> 1602

<212> PRT

<213> Plasmodium falciparum

<400> 7

Val	Thr	His	Glu	Ser	Tyr	Gln	Glu	Leu	Val	Lys	Lys	Leu	Glu	Ala	Leu
1				5					10					15	
Glu	Asp	Ala	Val	Leu	Thr	Gly	Tyr	Ser	Leu	Phe	Gln	Lys	Glu	Lys	Met
			20					25					30		
Val	Leu	Asn	Glu	Gly	Thr	Ser	Gly	Thr	Ala	Val	Thr	Thr	Ser	Thr	Pro
		35					40					45			
Gly	Ser	Lys	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Val	Ala
	50					55					60				
Ser	Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser	Val	Ala	Ser	Gly	Gly	Ser
65					70					75					80
Val	Ala	Ser	Gly	Gly	Ser	Gly	Asn	Ser	Arg	Arg	Thr	Asn	Pro	Ser	Asp
				85					90					95	
Asn	Ser	Ser	Asp	Ser	Asp	Ala	Lys	Ser	Tyr	Ala	Asp	Leu	Lys	His	Arg
			100					105					110		
Val	Arg	Asn	Tyr	Leu	Leu	Thr	Ile	Lys	Glu	Leu	Lys	Tyr	Pro	Gln	Leu
		115					120					125			
Phe	Asp	Leu	Thr	Asn	His	Met	Leu	Thr	Leu	Cys	Asp	Asn	Ile	His	Gly
	130					135					140				
Phe	Lys	Tyr	Leu	Ile	Asp	Gly	Tyr	Glu	Glu	Ile	Asn	Glu	Leu	Leu	Tyr
145					150					155					160
Lys	Leu	Asn	Phe	Tyr	Phe	Asp	Leu	Leu	Arg	Ala	Lys	Leu	Asn	Asp	Val
			165						170					175	
Cys	Ala	Asn	Asp	Tyr	Cys	Gln	Ile	Pro	Phe	Asn	Leu	Lys	Ile	Arg	Ala
		180						185					190		
Asn	Glu	Leu	Asp	Val	Leu	Lys	Lys	Leu	Val	Phe	Gly	Tyr	Arg	Lys	Pro
		195					200					205			
Leu	Asp	Asn	Ile	Lys	Asp	Asn	Val	Gly	Lys	Met	Glu	Asp	Tyr	Ile	Lys
	210					215					220				
Lys	Asn	Lys	Lys	Thr	Ile	Glu	Asn	Ile	Asn	Glu	Leu	Ile	Glu	Glu	Ser
225					230					235					240
Lys	Lys	Thr	Ile	Asp	Lys	Asn	Lys	Asn	Ala	Thr	Lys	Glu	Glu	Glu	Lys
			245						250					255	
Lys	Lys	Leu	Tyr	Gln	Ala	Gln	Tyr	Asp	Leu	Ser	Ile	Tyr	Asn	Lys	Gln
		260						265					270		
Leu	Glu	Glu	Ala	His	Asn	Leu	Ile	Ser	Val	Leu	Glu	Lys	Arg	Ile	Asp
	275						280						285		
Thr	Leu	Lys	Lys	Asn	Glu	Asn	Ile	Lys	Glu	Leu	Leu	Asp	Lys	Ile	Asn
	290					295					300				
Glu	Ile	Lys	Asn	Pro	Pro	Pro	Ala	Asn	Ser	Gly	Asn	Thr	Pro	Asn	Thr
305					310					315					320
Leu	Leu	Asp	Lys	Asn	Lys	Lys	Ile	Glu	Glu	His	Glu	Lys	Glu	Ile	Lys
			325						330					335	
Glu	Ile	Ala	Lys	Thr	Ile	Lys	Phe	Asn	Ile	Asp	Ser	Leu	Phe	Thr	Asp
		340						345					350		

Pro	Leu	Glu	Leu	Glu	Tyr	Tyr	Leu	Arg	Glu	Lys	Asn	Lys	Asn	Ile	Asp	355	360	365
Ile	Ser	Ala	Lys	Val	Glu	Thr	Lys	Glu	Ser	Thr	Glu	Pro	Asn	Glu	Tyr	370	375	380
Pro	Asn	Gly	Val	Thr	Tyr	Pro	Leu	Ser	Tyr	Asn	Asp	Ile	Asn	Asn	Ala	385	390	400
Leu	Asn	Glu	Leu	Asn	Ser	Phe	Gly	Asp	Leu	Ile	Asn	Pro	Phe	Asp	Tyr	405	410	415
Thr	Lys	Glu	Pro	Ser	Lys	Asn	Ile	Tyr	Thr	Asp	Asn	Glu	Arg	Lys	Lys	420	425	430
Phe	Ile	Asn	Glu	Ile	Lys	Glu	Lys	Ile	Lys	Ile	Glu	Lys	Lys	Lys	Ile	435	440	445
Glu	Ser	Asp	Lys	Lys	Ser	Tyr	Glu	Asp	Arg	Ser	Lys	Ser	Leu	Asn	Asp	450	455	460
Ile	Thr	Lys	Glu	Tyr	Glu	Lys	Leu	Leu	Asn	Glu	Ile	Tyr	Asp	Ser	Lys	465	470	475
Phe	Asn	Asn	Asn	Ile	Asp	Leu	Thr	Asn	Phe	Glu	Lys	Met	Met	Gly	Lys	485	490	495
Arg	Tyr	Ser	Tyr	Lys	Val	Glu	Lys	Leu	Thr	His	His	Asn	Thr	Phe	Ala	500	505	510
Ser	Tyr	Glu	Asn	Ser	Lys	His	Asn	Leu	Glu	Lys	Leu	Thr	Lys	Ala	Leu	515	520	525
Lys	Tyr	Met	Glu	Asp	Tyr	Ser	Leu	Arg	Asn	Ile	Val	Val	Glu	Lys	Glu	530	535	540
Leu	Lys	Tyr	Tyr	Lys	Asn	Leu	Ile	Ser	Lys	Ile	Glu	Asn	Glu	Ile	Glu	545	550	555
Thr	Leu	Val	Glu	Asn	Ile	Lys	Lys	Asp	Glu	Glu	Gln	Leu	Phe	Glu	Lys	565	570	575
Lys	Ile	Thr	Lys	Asp	Glu	Asn	Lys	Pro	Asp	Glu	Lys	Ile	Leu	Glu	Val	580	585	590
Ser	Asp	Ile	Val	Lys	Val	Gln	Val	Gln	Lys	Val	Leu	Leu	Met	Asn	Lys	595	600	605
Ile	Asp	Glu	Leu	Lys	Lys	Thr	Gln	Leu	Ile	Leu	Lys	Asn	Val	Glu	Leu	610	615	620
Lys	His	Asn	Ile	His	Val	Pro	Asn	Ser	Tyr	Lys	Gln	Glu	Asn	Lys	Gln	625	630	635
Glu	Pro	Tyr	Tyr	Leu	Ile	Val	Leu	Lys	Lys	Glu	Ile	Asp	Lys	Leu	Lys	645	650	655
Val	Phe	Met	Pro	Lys	Val	Glu	Ser	Leu	Ile	Asn	Glu	Glu	Lys	Lys	Asn	660	665	670
Ile	Lys	Thr	Glu	Gly	Gln	Ser	Asp	Asn	Ser	Glu	Pro	Ser	Thr	Glu	Gly	675	680	685
Glu	Ile	Thr	Gly	Gln	Ala	Thr	Thr	Lys	Pro	Gly	Gln	Gln	Ala	Gly	Ser	690	695	700
Ala	Leu	Glu	Gly	Asp	Ser	Val	Gln	Ala	Gln	Ala	Gln	Glu	Gln	Lys	Gln	705	710	715
Ala	Gln	Pro	Pro	Val	Pro	Val	Pro	Val	Pro	Glu	Ala	Lys	Ala	Gln	Val	725	730	735
Pro	Thr	Pro	Pro	Ala	Pro	Val	Asn	Asn	Lys	Thr	Glu	Asn	Val	Ser	Lys	740	745	750
Leu	Asp	Tyr	Leu	Glu	Lys	Leu	Tyr	Glu	Phe	Leu	Asn	Thr	Ser	Tyr	Ile	755	760	765
Cys	His	Lys	Tyr	Ile	Leu	Val	Ser	His	Ser	Thr	Met	Asn	Glu	Lys	Ile	770	775	780
Leu	Lys	Gln	Tyr	Lys	Ile	Thr	Lys	Glu	Glu	Glu	Ser	Lys	Leu	Ser	Ser	785	790	795
Cys	Asp	Pro	Leu	Asp	Leu	Leu	Phe	Asn	Ile	Gln	Asn	Asn	Ile	Pro	Val			

				805					810					815			
Met	Tyr	Ser	Met	Phe	Asp	Ser	Leu	Asn	Asn	Ser	Leu	Ser	Gln	Leu	Phe		
			820					825					830				
Met	Glu	Ile	Tyr	Glu	Lys	Glu	Met	Val	Cys	Asn	Leu	Tyr	Lys	Leu	Lys		
		835					840					845					
Asp	Asn	Asp	Lys	Ile	Lys	Asn	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Val	Ser		
	850					855					860						
Thr	Ser	Val	Lys	Thr	Leu	Ser	Ser	Ser	Ser	Met	Gln	Pro	Leu	Ser	Leu		
865					870					875					880		
Thr	Pro	Gln	Asp	Lys	Pro	Glu	Val	Ser	Ala	Asn	Asp	Asp	Thr	Ser	His		
			885						890					895			
Ser	Thr	Asn	Leu	Asn	Asn	Ser	Leu	Lys	Leu	Phe	Glu	Asn	Ile	Leu	Ser		
		900						905					910				
Leu	Gly	Lys	Asn	Lys	Asn	Ile	Tyr	Gln	Glu	Leu	Ile	Gly	Gln	Lys	Ser		
	915						920					925					
Ser	Glu	Asn	Phe	Tyr	Glu	Lys	Ile	Leu	Lys	Asp	Ser	Asp	Thr	Phe	Tyr		
	930					935					940						
Asn	Glu	Ser	Phe	Thr	Asn	Phe	Val	Lys	Ser	Lys	Ala	Asp	Asp	Ile	Asn		
945					950					955					960		
Ser	Leu	Asn	Asp	Glu	Ser	Lys	Arg	Lys	Lys	Leu	Glu	Glu	Asp	Ile	Asn		
			965					970						975			
Lys	Leu	Lys	Lys	Thr	Leu	Gln	Leu	Ser	Phe	Asp	Leu	Tyr	Asn	Lys	Tyr		
			980					985					990				
Lys	Leu	Lys	Leu	Glu	Arg	Leu	Phe	Asp	Lys	Lys	Lys	Thr	Val	Gly	Lys		
	995						1000					1005					
Tyr	Lys	Met	Gln	Ile	Lys	Lys	Leu	Thr	Leu	Leu	Lys	Glu	Gln	Leu	Glu		
	1010					1015					1020						
Ser	Lys	Leu	Asn	Ser	Leu	Asn	Asn	Pro	Lys	His	Val	Leu	Gln	Asn	Phe		
1025				1030						1035					1040		
Ser	Val	Phe	Phe	Asn	Lys	Lys	Lys	Glu	Ala	Glu	Ile	Ala	Glu	Thr	Glu		
			1045					1050						1055			
Asn	Thr	Leu	Glu	Asn	Thr	Lys	Ile	Leu	Leu	Lys	His	Tyr	Lys	Gly	Leu		
			1060					1065					1070				
Val	Lys	Tyr	Tyr	Asn	Gly	Glu	Ser	Ser	Pro	Leu	Lys	Thr	Leu	Ser	Glu		
	1075					1080					1085						
Glu	Ser	Ile	Gln	Thr	Glu	Asp	Asn	Tyr	Ala	Ser	Leu	Glu	Asn	Phe	Lys		
	1090					1095					1100						
Val	Leu	Ser	Lys	Leu	Glu	Gly	Lys	Leu	Lys	Asp	Asn	Leu	Asn	Leu	Glu		
1105					1110					1115					1120		
Lys	Lys	Lys	Leu	Ser	Tyr	Leu	Ser	Ser	Gly	Leu	His	His	Leu	Ile	Ala		
			1125						1130					1135			
Glu	Leu	Lys	Glu	Val	Ile	Lys	Asn	Lys	Asn	Tyr	Thr	Gly	Asn	Ser	Pro		
			1140					1145					1150				
Ser	Glu	Asn	Asn	Thr	Asp	Val	Asn	Asn	Ala	Leu	Glu	Ser	Tyr	Lys	Lys		
	1155					1160					1165						
Phe	Leu	Pro	Glu	Gly	Thr	Asp	Val	Ala	Thr	Val	Val	Ser	Glu	Ser	Gly		
	1170					1175					1180						
Ser	Asp	Thr	Leu	Glu	Gln	Ser	Gln	Pro	Lys	Lys	Pro	Ala	Ser	Thr	His		
1185					1190					1195					1200		
Val	Gly	Ala	Glu	Ser	Asn	Thr	Ile	Thr	Thr	Ser	Gln	Asn	Val	Asp	Asp		
			1205						1210					1215			
Glu	Val	Asp	Asp	Val	Ile	Ile	Val	Pro	Ile	Phe	Gly	Glu	Ser	Glu	Glu		
			1220					1225					1230				
Asp	Tyr	Asp	Asp	Leu	Gly	Gln	Val	Val	Thr	Gly	Glu	Ala	Val	Thr	Pro		
	1235					1240					1245						
Ser	Val	Ile	Asp	Asn	Ile	Leu	Ser	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Val		
	1250					1255					1260						

Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu Lys Lys Gln																			
1265					1270			1275											1280
Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys Asp Ile Leu																			
				1285				1290											1295
Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val Leu Glu Ser																			
			1300					1305											1310
Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr Val Val Lys																			
			1315					1320											1325
Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys Phe Leu Ser																			
			1330					1335											1340
Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile Asn Phe Ala																			
			1345					1350											1355
Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys Tyr Lys Ser																			
			1365																1370
Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln Gly Glu Asn																			
			1380																1385
Glu Lys Tyr Leu Pro Phe Leu Asn Ile Glu Thr Leu Tyr Lys Thr																			
			1395																1400
Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu Ala Lys Val																			
			1410																1415
Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys Ile Lys Glu																			
			1425																1430
Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp Phe Lys Lys																			
			1445																1450
Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp Tyr Asn His																			
			1460																1465
Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val Phe Glu Asn																			
			1475																1480
Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn Leu Gln Gly																			
			1490																1495
Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Gln																			
			1505																1510
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys																			
			1525																1530
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn																			
			1540																1545
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys																			
			1555																1560
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys																			
			1570																1575
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser																			
			1585																1590
Ser Asn																			1595
																			1600

<210> 8
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide

<400> 8
 Met Arg Gly Ser His His His His His His Gly Ser
 1 5 10